

Figure 1

TTTGTGGAGGGCAGCAGAGAGTACCCAGCTGGACATCCTTTCTGCTGATGAGCCCCAGGCTGGAGGTGCCCTGCTCACATGCTCTTCCC  
 90  
 AAACACCTCCCGTCGTCTCTCATGGGTCGACCTGTAGGAAAGGACGACTACTCGGGGTCCGACCTCCACGGGACGAGTGTACGAGAAGGG  
 M S P R L E V P C S H A L P  
 CAGGGTCTCTCGCCTGGGCAGGTCATCATAGTACGGGGACTGGTCTTGCAAGAGCCGAAGCATTTTACTGTGAGCCTGAGGGACCAGGCT  
 180  
 GTCCCAGAGAGCGGACCCGTCCAGTAGTATCATGCCCTGACCAGAACGTTCTCGGCTTCGTAAAATGACACTCGGACTCCCTGGTCCGA  
 Q G L S P G Q V I I V R G L V L Q E P K H F T V S L R D Q A  
 GCCCATGCTCCTGTGACACTCAGGGCCTCCTTCGCAGACAGAACTCTGGCCTGGATCTCCCGCTGGGGGCAGAAGAACTGATCTCAGCC  
 270  
 CGGGTACGAGGACACTGTGAGTCCCGGAGGAAGCGTCTGTCTTGAGACCGGACCTAGAGGGCGACCCCGTCTTCTTTGACTAGAGTCGG  
 A H A P V T L R A S F A Q R T L A W I S R W G Q K K L I S A  
 CCCTTCTCTTTTACCCCCAGAGATTCTTTGAGGTGCTGCTCCTGTTCCAGGAGGGAGGGCTGAAGCTGGCGCTCAATGGGCAGGGGCTG  
 360  
 GGAAGGAGAAAAATGGGGTCTCTAAGAACTCCACGACGAGGACAAGGTCTCCTCCCTCCCGACTTCGACCGCGAGTTAECGGTCCCCGAC  
 F L F Y P Q R F F E V L L L F Q E G G L K L A L N G Q G L  
 GGGGCCACCAGCATGAACCAGCAGGCCCTGGAGCAGCTGCGGGAGCTCCGGATCAGTGAAGTGTCCAGCTCTACTGTGTCCACTCCTGA  
 450  
 CCGGTGGTTCGTACTTGGTTCGTCCGGGACCTCGTCGACGCCCTCGAGGCCTAGTCACCTTCACAGGTGAGATGACACAGGTGAGGACT  
 A T S M N Q Q A L E Q L R E L R I S G S V Q L Y C V H S  
 AGATGGTTCCAGGAAATACCGCAGAAAACAAGAGTCAGCCACTCCCAGGGCCCCACTCTCCTCCCTCATTAAACCATCCACCTGAAC  
 540  
 CCTACCAAGGTCTTTATGGCGTCTTTGTTCTCAGTCGGTGAGGGGTCCCGGGTGAGAGGAGGGGAGTAATTTGGTAGGTGGAAGT  
 ACCAGCACATCAGGGCCTGGTTACCTCTGGGGTCACGAGACTGAGTCTACAGGAGCTTTGGGCCTGAGGGAAGGCACAAGAGTGCAAAG  
 630  
 TGGTCGTGTAGTCCCGGACCAAGTGGAGACCCAGTGTCTGACTCAGATGTCTCGAAACCCGGACTCCCTTCCGTGTTCTCACGTTTC  
 GTTCCTCGAACTCTGCACCTTCCTCCACCAGGAGCCTGGGATATGGCTCCATCTGCCTTCAGGGCCTGGACTGCACTCACAGAGGCAAGT  
 720  
 CAAGGAGCTTGAGACGTGGAAGGAGGTGGTCTCGGACCCTATACCGAGGTAGACGGAAGTCCCGGACCTGACGTGAGTGTCTCCGTTCA  
 GTTGTAGACTAACAAAGATACTCCAAAATACAATGGCTTAAAGAATGTGGTCATTTATTCTTTATTATTTATTTATTTGTGGTCAAATAA  
 810  
 CAACATCTGATTGTTTCTATGAGGTTTTATGTTACCGAATTTCTTACACCAGTAAATAAGAAATAATAAAATAAAACACCAAGTTTATT  
 ATAAATAAGGTTATTTATTTAAAAA  
 865  
 TATTTATTCCAATAAAATTTT

FIGURE 2

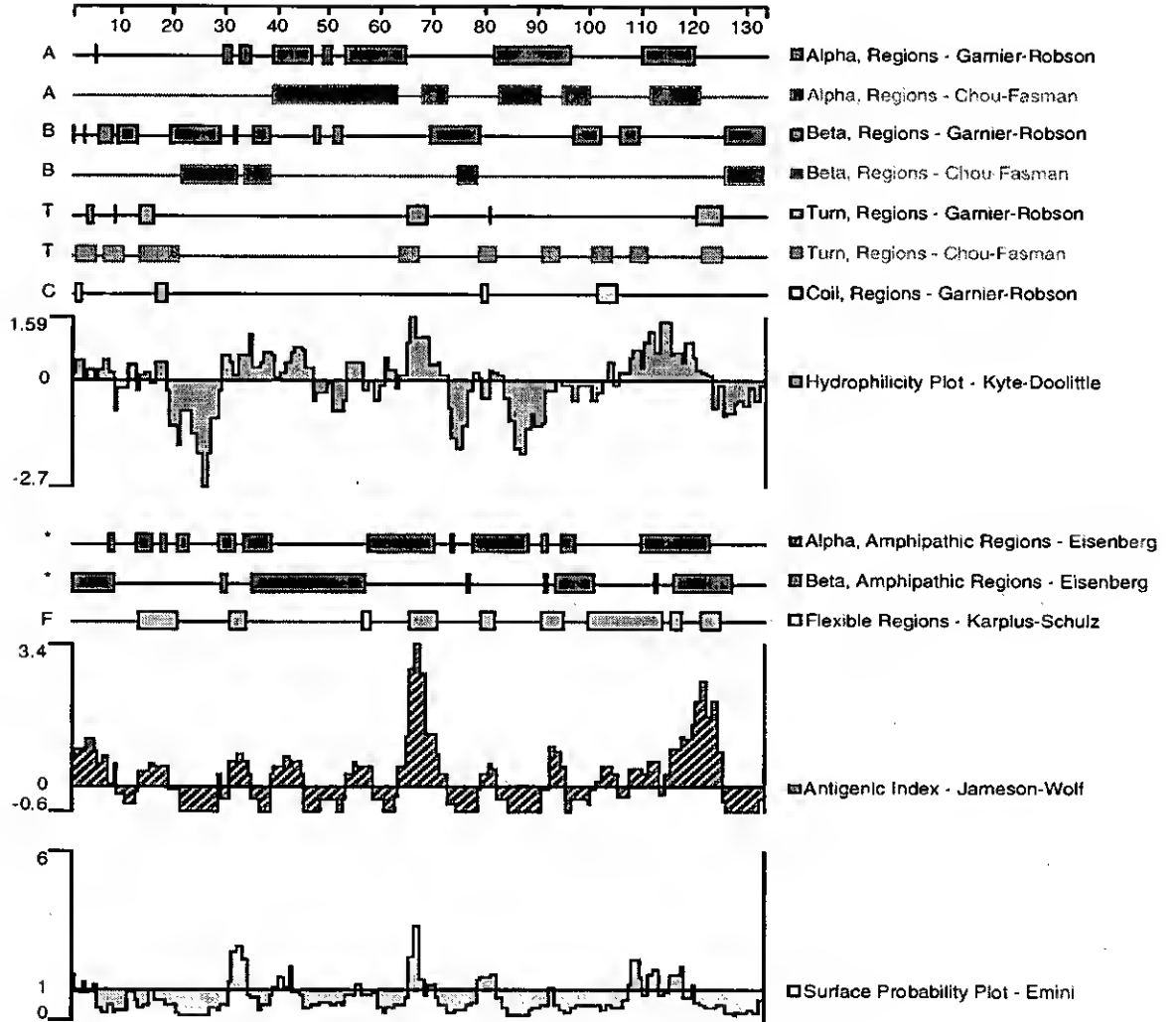
		10		20		30		40																																				
1	M	S	-	-	-	-	-	F	R	L	E	-	-	-	-	-	-	V	P	C	S	H	A	L	P	Q	G	L	S	P	G	Q	V	HJACE54.aa										
1	M	S	S	F	S	T	Q	T	P	Y	F	N	L	A	-	-	-	-	V	P	F	F	T	S	I	P	N	G	L	Y	P	S	K	S	rGalectin-5.aa									
1	M	M	-	-	-	-	-	-	-	-	L	S	L	N	N	L	Q	N	I	I	Y	N	P	V	I	P	F	V	G	T	I	P	N	G	L	Y	P	S	K	S	hGalectin-8.aa			
																																					</							

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

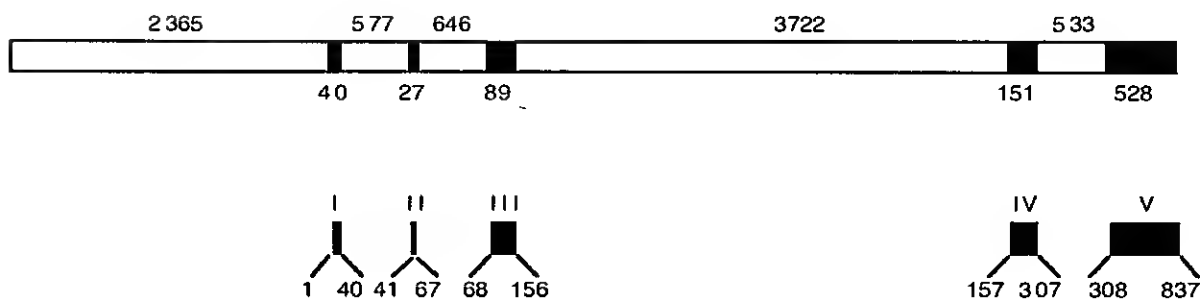
09109864.070698

FIGURE 3



09109864-070698

FIGURE 4



069020"49860760

FIGURE 5A

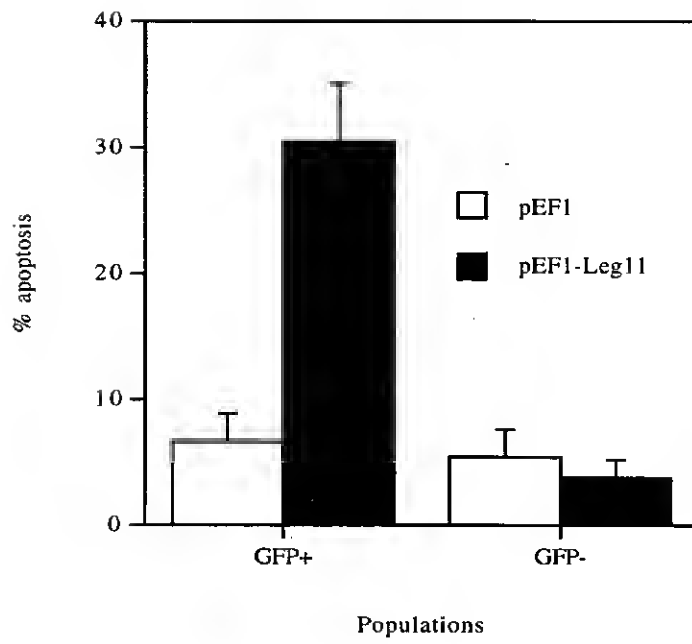
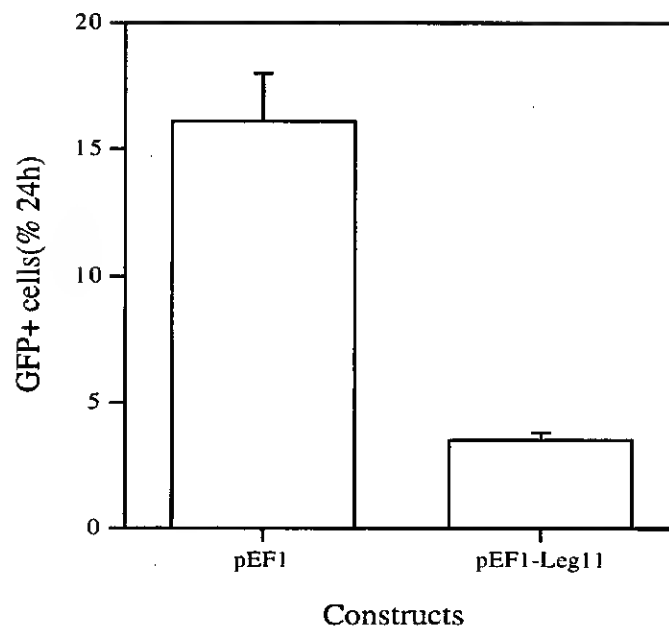


FIGURE 5B



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